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☐ 1: Q16853. Reports Membrane copper a...

BLink, Domains,

[gi:2501336]

Links

LOCUS Q16853 763 aa linear PRI 15-JUN-2004
 DEFINITION Membrane copper amine oxidase (Vascular adhesion protein-1) (VAP-1) (HPAO).
 ACCESSION Q16853
 VERSION Q16853 GI:2501336
 DBSOURCE swissprot: locus AOC3_HUMAN, accession Q16853;
 class: standard.
 created: Nov 1, 1997.
 sequence updated: Nov 1, 1997.
 annotation updated: Jun 15, 2004.
 xrefs: gi: [1399031](#), gi: [1399032](#), gi: [3283369](#), gi: [3283370](#), gi: [11602472](#), gi: [11602473](#), gi: [11602470](#), gi: [11602471](#), gi: [29792246](#), gi: [29792247](#), gi: [2134747](#)
 xrefs (non-sequence databases): GenewHGNC:550, MIM 603735, GO0016021, GO0005886, GO0008122, GO0005489, GO0009308, InterProIPR000269, PfamPF01179, PfamPF02727, PfamPF02728, PRINTSPR00766, PROSITEPS01164, PROSITEPS01165
 KEYWORDS Oxidoreductase; Copper; TPQ; Glycoprotein; Transmembrane; Signal-anchor; Cell adhesion; Polymorphism; Metal-binding; Direct protein sequencing.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 763)
 AUTHORS Zhang,X. and McIntire,W.S.
 TITLE Cloning and sequencing of a copper-containing, topa quinone-containing monoamine oxidase from human placenta
 JOURNAL Gene 179 (2), 279-286 (1996)
 MEDLINE 97128319
 PUBMED 8972912
 REMARK SEQUENCE FROM N.A.
 TISSUE=Placenta
 REFERENCE 2 (residues 1 to 763)
 AUTHORS Smith,D.J., Salmi,M., Bono,P., Hellman,J., Leu,T. and Jalkanen,S.
 TITLE Cloning of vascular adhesion protein 1 reveals a novel multifunctional adhesion molecule
 JOURNAL J. Exp. Med. 188 (1), 17-27 (1998)
 MEDLINE 98317014
 PUBMED 9653080
 REMARK SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 TISSUE=Lung
 REFERENCE 3 (residues 1 to 763)
 AUTHORS Zhang,Q., Mashima,Y., Noda,S., Imamura,Y., Kudoh,J., Shimizu,N., Nishiyama,T., Umeda,S., Oguchi,Y., Tanaka,Y. and Iwata,T.
 TITLE Characterization of AOC2 gene encoding a copper-binding amine oxidase expressed specifically in retina
 JOURNAL Gene 318, 45-53 (2003)

MEDLINE 22948120
 PUBMED 14585497
 REMARK SEQUENCE FROM N.A.
 REFERENCE 4 (residues 1 to 763)
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 MEDLINE 22388257
 PUBMED 12477932
 REMARK SEQUENCE FROM N.A.
 TISSUE=PNS
 COMMENT -----
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. The original entry is available from <http://www.expasy.ch/sprot> and <http://www.ebi.ac.uk/sprot>

 [FUNCTION] Cell adhesion protein that participate in lymphocyte recirculation by mediating the binding of lymphocytes to peripheral lymph node vascular endothelial cells in an L-selectin-independent fashion. Has a monoamine oxidase activity.
 [CATALYTIC ACTIVITY] $\text{RCH(2)NH(2)} + \text{H(2)O} + \text{O(2)} = \text{RCHO} + \text{NH(3)} + \text{H(2)O(2)}$.
 [COFACTOR] Binds 1 copper ion and 1 topaquinone per subunit.
 [SUBUNIT] Homodimer.
 [SUBCELLULAR LOCATION] Type II membrane protein.
 [TISSUE SPECIFICITY] Most strongly expressed on the high endothelial venules of peripheral lymph nodes and on hepatic endothelia.
 [PTM] Topaquinone (TPQ) is generated by copper-dependent autoxidation of a specific tyrosyl residue (By similarity).
 [PTM] N- and O-glycosylated.
 [SIMILARITY] Belongs to the copper/topaquinone oxidase family.
 FEATURES Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 gene 1..763
 /gene="AOC3"
 /note="synonym: VAP1"
 Protein 1..763

Region /gene="AOC3"
 /product="Membrane copper amine oxidase"
 /EC_number="1.4.3.6"
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 /region_name="Domain"
 /note="Cytoplasmic (Potential)."
6..26
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 /region_name="Transmembrane region"
 /note="Signal-anchor for type II membrane protein
 (Potential)."
27..763
Region /gene="AOC3"
 /region_name="Domain"
 /note="Extracellular (Potential)."
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 /note="Cu_amine_oxidN2"
 /db_xref="CDD:3234"
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 /note="N-linked (GlcNAc...) (Potential)."
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 /region_name="Copper amine oxidase, N3 domain"
 /note="Cu_amine_oxidN3"
 /db_xref="CDD:6797"
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Site /gene="AOC3"
 /site_type="glycosylation"
 /note="N-linked (GlcNAc...) (Potential)."
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Site /gene="AOC3"
 /site_type="glycosylation"
 /note="N-linked (GlcNAc...) (Potential)."
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 /region_name="Copper amine oxidase, enzyme domain"
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 /db_xref="CDD:25702"
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592

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 /note="N-linked (GlcNAc...) (Potential)."
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 /note="N-linked (GlcNAc...) (Potential)."
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 /site_type="binding"
 /note="Amiloride (By similarity)."
684
 /gene="AOC3"
 /site_type="metal-binding"
 /note="Copper (Potential)."

ORIGIN

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1 mnqktilvll ilavitifal vcvllvgrgg dggepsqlph cpsvspsaqp wthpggsqqlf
61 adlsreelta vmrfltqrlg pglvd aaqar psdncv fsve lqlppkaaal ahldrgsppp
121 arealaivff grqpqp nvse lvvgplphps ymrdvt verh ggplpyhrrp vlfqeyldid
181 qmifnrelpq asgllhhccf ykhrgrnlvt mttaprglqs gdratwfgly ynissagffl
241 hhvglellvn hkaldparwt iqkvfyggry yds laqlea feaglvnvvl ipdngtggs w
301 slkspvp ppgp applqfypqg prfsvqgsrv asslwtfsfg lgafsgprif dvrfggerlv
361 yeislqeala iyggns paam ttryvdggfg mgk yttpltr gvdcpylaty vdwhfllesq
421 apktirdafc vfeqnqglpl rrhhsdlysh yfgglaetvl vvrsmstlln ydyvwdtvfh
481 psgaieirfy atgyiss afl fgatgkygnq vsehtlgtvh thsahfkvdl dvaglenwvw
541 aedmvfv pma vpwspehqlq rlqvtrk lle mee qaaf lvg satprylyla snhsnkwghp
601 rgyriqmlsf ageplpq nss margfswery qlavtqrkee epssssvf nq ndpwaptvdf
661 sdfinnetia gkd lvawvta gflhiphaed ipntvtvgng vgfflrpy nf fdedpsfysa
721 dsiyfrgdqd agacevnpla clpqaaacap dlpafshggf shn
```

//

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[NCBI](#) | [NLM](#) | [NIH](#)

Oct 29 2004 14:28:57

Database : SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3405	63.6	763	6	Q9TTK6	Q9ttk6 bos taurus
2	3370	62.9	765	11	Q9R055	Q9r055 mus musculu
3	3174	59.2	1640	11	Q7TP38	Q7tp38 rattus norv
4	2390.5	44.6	757	11	Q812C9	Q812c9 mus musculu
5	2389.5	44.6	757	11	Q80WP3	Q80wp3 mus musculu
6	1404.5	26.2	751	11	Q8VC36	Q8vc36 mus musculu
7	1403.5	26.2	751	11	Q8JZQ5	Q8jzq5 mus musculu
8	1032	19.3	447	11	Q8R229	Q8r229 mus musculu
9	1029	19.2	218	5	Q94745	Q94745 schistosoma
10	992	18.5	820	11	Q8BZI2	Q8bzi2 mus musculu
11	771.5	14.4	821	3	Q86ZN4	Q86zn4 podospora a
12	721	13.5	218	5	Q25595	Q25595 clonorchis
13	707	13.2	218	5	Q9XYL9	Q9xyl9 fasciola gi
14	649	12.1	787	3	Q96X16	Q96x16 pichia past
15	615.5	11.5	271	11	Q920K6	Q920k6 cavia porce
16	518.5	9.7	218	6	Q9N0V4	Q9n0v4 bos taurus
17	514.5	9.6	219	13	Q7SZ23	Q7sz23 xenopus lae
18	513.5	9.6	219	13	Q90WM9	Q90wm9 xenopus lae
19	507.5	9.5	218	11	Q8R5I6	Q8r5i6 mus musculu
20	503.5	9.4	223	5	O97117	O97117 boophilus m
21	484.5	9.0	218	6	Q9TSM5	Q9tsm5 macaca fasc
22	481.5	9.0	218	6	Q9TSM4	Q9tsm4 macaca fasc
23	481.5	9.0	221	6	Q9BEB0	Q9beb0 macaca fusc
24	479.5	9.0	218	11	Q91Y83	Q91y83 cavia porce
25	479.5	9.0	218	11	Q8K0C3	Q8k0c3 mus musculu
26	472.5	8.8	204	11	Q9CW16	Q9cw16 mus musculu
27	470.5	8.8	219	5	Q8MWS0	Q8mws0 taenia soli
28	468.5	8.7	218	11	Q9WU21	Q9wu21 rattus norv
29	466.5	8.7	218	11	Q80W21	Q80w21 mus musculu

30	463.5	8.7	219	5	Q27653	Q27653 echinococcu
31	462.5	8.6	219	5	O16058	O16058 echinococcu
32	462	8.6	133	11	Q8CH13	Q8ch13 rattus norv
33	455.5	8.5	225	4	Q96HA3	Q96ha3 homo sapien
34	449.5	8.4	225	6	Q9BEA9	Q9bea9 macaca fusc
35	441.5	8.2	232	11	Q9D5J8	Q9d5j8 mus musculu
36	440.5	8.2	225	11	Q9Z1B2	Q9z1b2 rattus norv
37	439.5	8.2	195	4	Q05465	Q05465 homo sapien
38	417.5	7.8	219	5	Q8I9R9	Q8i9r9 sarcoptes s
39	415.5	7.8	188	6	Q9MZB4	Q9mzb4 capra hircu
40	388	7.2	741	10	Q9C6V7	Q9c6v7 arabidopsis
41	386.5	7.2	219	5	Q9U582	Q9u582 psoroptes o
42	381	7.1	654	16	Q989X2	Q989x2 rhizobium l
43	372.5	7.0	668	10	O48552	O48552 arabidopsis
44	371.5	6.9	557	10	Q8GZ62	Q8gz62 arabidopsis
45	368.5	6.9	660	17	Q97XM1	Q97xm1 sulfolobus

ALIGNMENTS

RESULT 1

Q9TTK6

ID Q9TTK6 PRELIMINARY; PRT; 763 AA.
AC Q9TTK6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Semicarbazide-sensitive amine oxidase (EC 1.4.3.6) (Copper amine
DE oxidase).
GN SSAO.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Iwabuki H., Matsumura K., Mure M., Kuroda S., Tanizawa K.;
RT "Molecular cloning of semicarbazide-sensitive amine oxidase gene from
RT Bovine aorta."
RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- CATALYTIC ACTIVITY: RCH(2)NH(2) + H(2)O + O(2) = RCHO + NH(3) +
CC H(2)O(2).
CC -!- COFACTOR: BINDS 1 COPPER ION AND 1 TOPAQUINONE PER SUBUNIT (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE COPPER/TOPAQUINONE OXIDASE FAMILY.
DR EMBL; AB019242; BAA88896.1; -.
DR GO; GO:0008122; F:amine oxidase (copper-containing) activity; IEA.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR000269; CuNH_oxidase.
DR Pfam; PF01179; Cu_amine_oxid; 1.
DR Pfam; PF02727; Cu_amine_oxidN2; 1.
DR Pfam; PF02728; Cu_amine_oxidN3; 1.
DR PRINTS; PR00766; CUDAOXIDASE.
DR PROSITE; PS01164; COPPER_AMINE_OXID_1; 1.

DR PROSITE; PS01165; COPPER_AMINE_OXID_2; 1.
KW Copper; Oxidoreductase; TPQ.
SQ SEQUENCE 763 AA; 84500 MW; DB61ED9A89E71E90 CRC64;

Query Match 63.6%; Score 3405; DB 6; Length 763;
Best Local Similarity 85.1%; Pred. No. 1.2e-267;
Matches 626; Conservative 44; Mismatches 66; Indels 0; Gaps 0;

Qy	263	QGGDGGEPSQLPHCPSPSAQPWTHPGQSQLFADLSREELTAVMRFLTQRLGPGLVDAA	322
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Db	28	RGGDGGGEASQPHYCPSGTPSVQPWTHPGQNQLFADLSREELTAVMSFLTQKLGPDLDVDA	87
Qy	323	QARPSDNCVFSVELQLPPKAAALAHLDRGSPPPAREALAIVFFGRQPQPNVSELVVGPLP	382
		: :	
Db	88	QARPSDNCIFSVELQLPPKAAALAHLDRRSPPPAREALAIVFFGGQPQPNVTELVVGPLP	147
Qy	383	HPSYMRDVTVERHGGPLPYHRRPVLFQEYLDIDQMIFNRELPAASGLLHHCCFYKHRGRN	442
		: : :	
Db	148	QPSYMRDVTVERHGGPLPYRRPVLLREYLDIDQMIFNRELPAAGVLHHCCSYKQGGGN	207
Qy	443	LVTMTTAPRGLQSGDRATWFGLYYNISGAGFFLHHVGLELLVNHKALDPAWRTIQKVFIQ	502
		: : :	
Db	208	LVTMTTAPRGLQSGDRATWFGLYYNISGAGYYLHPVGLELLVDHKALDPAQWTIQKVFFQ	267
Qy	503	GRYYSLSLAQLEAQFEAGLVNVVLIIPDNGTGGSWSLKSPVPPGPAPPLQFYPPQGRFSVQG	562
		: : : :	
Db	268	GRYYESLAQLEEQFEAGRVNVVVIIPNNGTGGSWSLKSQVPPGPTPPLQFHPQGRFSVQG	327
Qy	563	SRVASSLWTFSGFLGAFSGPRIFDVRFQGERLVYEISLQEALAIYGGNSPAAMTTRYVDG	622
		: : :	
Db	328	SRVTSSLWTFSGFLGAFSGPRIFDIRFQGERLAYEISLQEAVAIYGGNTPAAMLTRYMDG	387
Qy	623	GFGMGKYTTPLTRGVDCPYLATYVDWHFLLESQAPKTIRDAFCVFEQNQGLPLRRHHSDDL	682
		: : : :	
Db	388	CFGMGKFATPLTRGVDCPYLATYVDWHFLLESQAPRTLHDAFCVFEQNKGLPLRRHHSDF	447
Qy	683	YSHYFGGLAETVLVVRSMSTLLNYDYVWDTVFHPSGAIEIRFYATGYISSAFLFGATGKY	742
		: : : : :	
Db	448	ISQYFGGVVETVLVFRSVSTLLNYDYVWDMVFPNGAIEVKFHATGYISSAFFFGTAQKY	507
Qy	743	GNQVSEHTLGTVHTHSAHFVLDVAGLENVWVAEDMVFPMAVPWSPPEHQLQRLQVTRK	802
		: : :	
Db	508	GNQVRENTLGTVHTHSAHYKVDLDVGLENVWVAEDMAFVPTTPWSPPEHQIQRLQVTRK	567
Qy	803	LLEMEEQAFLVGSATPRYLILASNSNKGHPRGYRIQMLSFAGEPLPQNSSMARGFSW	862
		: : :	
Db	568	QLETEEQAFLGASPRYLILASKQSNKGHPRGYRIQTVSFAGRPLPQNSSSTERAISW	627
Qy	863	ERYQLAVTQRKEEEPSSSSVFNQNDPWAPTVDVDFINNETIAGKDLVAWVTAGFLHIPH	922
		:	
Db	628	GRYQLAVTQRKETEPSSSSVFNQNDPWTPTVDVDFINNETIAGKDLVAWVTAGFLHIPH	687
Qy	923	AEDIPNTVTVGNGVGFFLRPNFFDEDPFYSADSIYFRGDQDAGACEVNPLACLPQAAA	982
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Db	688	AEDIPNTVTVGNGVGFFLRPNFFDEDPFINSADSIYFQKHQDAGSCEVNSLACLPKDPA	747
Qy	983	CAPDLPAFSGHGGFSHN	998

Db

|||||
748 CAPDLPAFSHGGFTN 763

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	3967	74.1	763	1	AOC3_HUMAN	Q16853	homo sapien
2	3365	62.8	765	1	AOC3_MOUSE	O70423	mus musculu
3	3338	62.3	762	1	AOCY_BOVIN	O46406	bos taurus
4	3326	62.1	762	1	AOCX_BOVIN	Q29437	bos taurus
5	2556	47.7	756	1	AOC2_HUMAN	O75106	homo sapien
6	1398.5	26.1	746	1	ABP_RAT	P36633	rattus norv
7	1394	26.0	751	1	ABP_HUMAN	P19801	homo sapien
8	1315	24.5	321	1	AOC3_RAT	O08590	rattus norv
9	1144	21.4	218	1	GT26_SCHJA	P08515	schistosoma
10	985	18.4	218	1	GT27_SCHMA	P35661	schistosoma
11	922	17.2	218	1	GT26_SCHMA	P15964	schistosoma
12	719.5	13.4	220	1	GT29_FASHE	P56598	fasciola he
13	708	13.2	217	1	GT27_FASHE	P31670	fasciola he
14	690	12.9	217	1	GT28_FASHE	P31671	fasciola he
15	689	12.9	217	1	GT26_FASHE	P30112	fasciola he
16	489.5	9.1	217	1	GTM1_MOUSE	P10649	mus musculu
17	489.5	9.1	217	1	GTM1_RAT	P04905	rattus norv
18	485.5	9.1	217	1	GTMU_RABIT	P46409	oryctolagus
19	485.5	9.1	218	1	GTM6_MOUSE	O35660	mus musculu
20	484.5	9.0	217	1	GTM2_HUMAN	P28161	homo sapien
21	483.5	9.0	218	1	GTM4_HUMAN	Q03013	homo sapien
22	481.5	9.0	217	1	GTMU_CAVPO	P16413	cavia porce
23	476.5	8.9	217	1	GTMU_CRILLO	Q00285	cricetulus
24	476.5	8.9	217	1	GTMU_MESAU	P30116	mesocricetu
25	475.5	8.9	217	1	GTM2_MOUSE	P15626	mus musculu
26	473.5	8.8	217	1	GTM1_HUMAN	P09488	homo sapien

Database : PIR_78:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	3967	74.1		763	2	JC5234	amine oxidase (cop
2	3326	62.1		762	2	A54411	amine oxidase (cop
3	1398.5	26.1		746	2	S34656	amine oxidase (cop
4	1394	26.0		751	2	A54053	amine oxidase (cop
5	1140	21.3		219	2	A26484	glutathione transf
6	985	18.4		218	2	A45556	glutathione S-tran
7	922	17.2		218	2	A45523	glutathione transf
8	663	12.4		209	2	A48388	glutathione S-tran
9	489.5	9.1		218	2	S33860	glutathione transf
10	489.5	9.1		218	2	A29794	glutathione transf
11	486.5	9.1		218	2	S32425	glutathione transf
12	485.5	9.1		218	2	S65674	glutathione transf
13	484.5	9.0		218	2	A39375	glutathione transf
14	483.5	9.0		218	2	A47486	glutathione transf
15	481.5	9.0		217	2	JX0095	glutathione transf
16	476.5	8.9		218	2	S13202	glutathione transf
17	476.5	8.9		218	2	A23732	glutathione transf
18	475.5	8.9		218	2	B34159	glutathione transf
19	473.5	8.8		218	2	S01719	glutathione transf
20	471.5	8.8		218	2	A46048	glutathione transf

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	5357	100.0	998	13	US-10-081-408-20	Sequence 20, Appl	
2	3967	74.1	763	13	US-10-081-408-2	Sequence 2, Appli	
3	2480.5	46.3	729	9	US-09-919-497-51	Sequence 51, Appl	
4	1368.5	25.5	770	16	US-10-408-765A-125	Sequence 125, App	
5	1184	22.1	504	14	US-10-050-902-289	Sequence 289, App	
6	1184	22.1	504	14	US-10-050-898-289	Sequence 289, App	
7	1179.5	22.0	419	14	US-10-050-902-318	Sequence 318, App	
8	1179.5	22.0	419	14	US-10-050-898-318	Sequence 318, App	
9	1176	22.0	692	15	US-10-318-308-1	Sequence 1, Appli	
10	1171.5	21.9	514	12	US-10-325-810-605	Sequence 605, App	

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	1180	22.0	447	4	US-08-506-296B-73	Sequence 73, Appl
2	1175.5	21.9	644	4	US-08-506-296B-65	Sequence 65, Appl
3	1175	21.9	536	3	US-08-974-180-20	Sequence 20, Appl
4	1171.5	21.9	514	3	US-08-974-549A-605	Sequence 605, App
5	1171.5	21.9	514	4	US-08-912-951-319	Sequence 319, App
6	1171.5	21.9	514	4	US-09-402-181B-605	Sequence 605, App
7	1171.5	21.9	514	4	US-09-721-456-605	Sequence 605, App
8	1168	21.8	1252	4	US-10-012-762-20	Sequence 20, Appl
9	1168	21.8	1252	4	US-09-704-036B-20	Sequence 20, Appl
10	1167.5	21.8	362	1	US-08-395-507-2	Sequence 2, Appli
11	1165	21.7	517	3	US-08-974-549A-606	Sequence 606, App
12	1165	21.7	517	4	US-08-912-951-320	Sequence 320, App
13	1165	21.7	517	4	US-09-402-181B-606	Sequence 606, App
14	1165	21.7	517	4	US-09-721-456-606	Sequence 606, App
15	1164.5	21.7	443	4	US-08-506-296B-76	Sequence 76, Appl

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	5357	100.0	998	5	AAE26690	Aae26690 S. japoni
2	3967	74.1	763	2	AAAY03219	Aay03219 Amino aci
3	3967	74.1	763	5	AAE26686	Aae26686 Human sem
4	2480.5	46.3	729	5	AAU84261	Aau84261 Human end
5	1398.5	26.1	746	7	ADE64055	Ade64055 Rat Prote
6	1394	26.0	751	7	ADE64057	Ade64057 Human Pro
7	1184	22.1	504	5	ABG94324	Abg94324 Lymphotox
8	1184	22.1	504	5	ABG80636	Abg80636 Mouse lym
9	1182.5	22.1	697	7	ADE52287	Ade52287 Human GST
10	1180	22.0	447	5	AAU10670	Aau10670 Mouse L1C
11	1179.5	22.0	419	5	ABG94337	Abg94337 GST-PS-C-
12	1179.5	22.0	419	5	ABG80649	Abg80649 Mouse RAN
13	1176.5	22.0	843	7	ADC51505	Adc51505 Human GST

RESULT 2

AA03219

ID AA03219 standard; protein; 763 AA.

XX

AC AA03219;

XX

DT 21-JUN-1999 (first entry)

XX

DE Amino acid sequence of the vascular adhesion protein-1.

XX

KW Human; vascular adhesion protein-1; VAP-1; endothelial cell; lymphocyte;
 KW inhibition; amine oxidase.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Peptide	1. .25
----	---------	--------

FT		/note= "N-terminal tryptic peptide"
----	--	-------------------------------------

FT	Domain	5. .27
----	--------	--------

FT		/note= "transmembrane domain"
----	--	-------------------------------

FT	Misc-difference	43
----	-----------------	----

FT		/note= "potential O-glycosylation site"
----	--	---

FT	Misc-difference	47
----	-----------------	----

FT		/note= "potential O-glycosylation site"
----	--	---

FT	Peptide	74. .78
----	---------	---------

FT		/note= "V8 peptide"
----	--	---------------------

FT	Misc-difference	137
----	-----------------	-----

FT		/note= "potential N-glycosylation site"
----	--	---

FT	Peptide	170. .174
----	---------	-----------

FT		/note= "V8 peptide"
----	--	---------------------

FT	Misc-difference	232
----	-----------------	-----

FT		/note= "potential N-glycosylation site"
----	--	---

FT	Peptide	259. .262
----	---------	-----------

FT		/note= "V8 peptide"
----	--	---------------------

FT	Peptide	264. .277
----	---------	-----------

FT		/note= "V8 peptide"
----	--	---------------------

FT	Misc-difference	294
----	-----------------	-----

FT		/note= "potential N-glycosylation site"
----	--	---

FT	Peptide	323. .329
----	---------	-----------

FT		/note= "V8 peptide"
----	--	---------------------

FT	Peptide	359. .361
----	---------	-----------

FT		/note= "V8 peptide"
----	--	---------------------

FT	Peptide	368. .375
----	---------	-----------

FT		/note= "V8 peptide"
----	--	---------------------

FT	Peptide	384. .393
----	---------	-----------

FT		/note= "V8 peptide"
----	--	---------------------

FT	Peptide	562. .566
----	---------	-----------

FT		/note= "V8 peptide"
----	--	---------------------

FT	Misc-difference	592
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FT		/note= "potential N-glycosylation site"
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FT	Peptide	597. .601
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FT		/note= "V8 peptide"
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FT	Misc-difference	618
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FT		/note= "potential N-glycosylation site"
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FT	Peptide	624. .637
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FT		/note= "V8 peptide"
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FT	Misc-difference	666
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FT      /note= "potential N-glycosylation site"
FT      Misc-difference 679
FT      /note= "potential O-glycosylation site"
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PN      WO9853049-A1.
XX
PD      26-NOV-1998.
XX
PF      22-MAY-1998;    98WO-FI000429.
XX
PR      23-MAY-1997;    97US-00862433.
XX
PA      (BIOT-) BIOTIE THERAPIES LTD.
XX
PI      Jalkanen S,  Salmi M,  Smith DJ,  Bono P;
XX
DR      WPI; 1999-131690/11.
DR      N-PSDB; AAX28632.
XX
PT      Nucleic acid encoding a novel human endothelial cell adhesion protein
PT      designated VAP-1 - having an adhesive function and an amine oxidase
PT      function useful for manipulating VAP-1 mediated binding of endothelial
PT      cells to lymphocytes.
XX
PS      Claim 1; Fig 1; 66pp; English.
XX
CC      This is the nucleotide sequence encoding the human vascular adhesion
CC      protein-1 (VAP-1) used in the method of the invention. The method
CC      involves manipulating VAP-1 mediated binding of endothelial cells to
CC      lymphocytes which comprises inhibiting the enzymatic activity of amine
CC      oxidase in endothelial cells, and potentiating the enzymatic activity of
CC      endothelial cells
XX
SQ      Sequence 763 AA;

Query Match          74.1%;  Score 3967;  DB 2;  Length 763;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 735;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      263 QGGDGGEP SQLPHCPSVSPSAQPWTHPGQSQLFADLSREELTAVMRFLTQRLGPGLVDAA 322
      :|||||
Db      28  RGGDGGEP SQLPHCPSVSPSAQPWTHPGQSQLFADLSREELTAVMRFLTQRLGPGLVDAA 87

Qy      323 QARPSDNCVFSVELQLPPKAAALHLDRGSPPPAREALAI VFFGRQPQPNVSELVVGPLP 382
      ||||||
Db      88  QARPSDNCVFSVELQLPPKAAALHLDRGSPPPAREALAI VFFGRQPQPNVSELVVGPLP 147

Qy      383 HPSYMRDVTVERHGGPLPYHRRPVLFQEYLDIDQMIFNREL PQASGLLHHCCFYKHRGRN 442
      ||||||
Db      148 HPSYMRDVTVERHGGPLPYHRRPVLFQEYLDIDQMIFNREL PQASGLLHHCCFYKHRGRN 207

Qy      443 LVTMTTAPRGLQSGDRATWFGLYYNISGAGFFLHHVGLELLVNHKALDPARWTIQKVFYQ 502
      ||||||
Db      208 LVTMTTAPRGLQSGDRATWFGLYYNISGAGFFLHHVGLELLVNHKALDPARWTIQKVFYQ 267

Qy      503 GRYYDSLAQLEAQFEAGLVNVVLIPDNGTGGSWSLKSPVPPGPAPPLQFYYPQGRFSVQG 562
      ||||||

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Db	268	GRYYDSLAQLEAQFEAGLVNVVLI	PDNGTGGSWSLKSPVPPGPAPPLQFYPQGPRFSVQG	327
Qy	563	SRVASSLWTF	SFGLGAFSGPRIFDVRFQGERLVYEISLQEALAIYGGNSPAAMTTRYVDG	622
Db	328	SRVASSLWTF	SFGLGAFSGPRIFDVRFQGERLVYEISLQEALAIYGGNSPAAMTTRYVDG	387
Qy	623	GFGMGKYTTPLTRGVDCPYLATYVDWHFLL	ESQAPKTIRDAFCVFEQNQGLPLRRHSDL	682
Db	388	GFGMGKYTTPLTRGVDCPYLATYVDWHFLL	ESQAPKTIRDAFCVFEQNQGLPLRRHSDL	447
Qy	683	YSHYFGGLAETVLVVRSMSTLLNYDYVWD	TVFHPSGAIEIRFYATGYISSAFLFGATGKY	742
Db	448	YSHYFGGLAETVLVVRSMSTLLNYDYVWD	TVFHPSGAIEIRFYATGYISSAFLFGATGKY	507
Qy	743	GNQVSEHTLGTVHTSAHFKVDLDVAGLEN	NWVWAEDMVFPMAVPWSPEHQLQRLQVTRK	802
Db	508	GNQVSEHTLGTVHTSAHFKVDLDVAGLEN	NWVWAEDMVFPMAVPWSPEHQLQRLQVTRK	567
Qy	803	LLEMEEQAAFLVGSATPRYLYLASNHSNK	WGHPRGYRIQMLSFAGEPLPQNSSMARGFSW	862
Db	568	LLEMEEQAAFLVGSATPRYLYLASNHSNK	WGHPRGYRIQMLSFAGEPLPQNSSMARGFSW	627
Qy	863	ERYQLAVTQRKEEPPSSSSVFNQNDPWAPT	VDFSDFINNETIAGKDLVAWVTAGFLHIPH	922
Db	628	ERYQLAVTQRKEEPPSSSSVFNQNDPWAPT	VDFSDFINNETIAGKDLVAWVTAGFLHIPH	687
Qy	923	AEDIPNTVTVGNGVGFFLRPYNFFDEDPS	FYSADSIYFRGDQDAGACEVNPLACLQAAA	982
Db	688	AEDIPNTVTVGNGVGFFLRPYNFFDEDPS	FYSADSIYFRGDQDAGACEVNPLACLQAAA	747
Qy	983	CAPDLPAFSHGGFSHN		998
Db	748	CAPDLPAFSHGGFSHN		763

RESULT 1

AOC3_HUMAN

ID AOC3_HUMAN STANDARD; PRT; 763 AA.
AC Q16853;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Membrane copper amine oxidase (EC 1.4.3.6) (Vascular adhesion protein-
DE 1) (VAP-1) (HPAO).
GN AOC3 OR VAP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=97128319; PubMed=8972912;
RA Zhang X., McIntire W.S.;
RT "Cloning and sequencing of a copper-containing, topaquinone-
RT containing monoamine oxidase from human placenta.";
RL Gene 179:279-286(1996).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=98317014; PubMed=9653080;
RA Smith D.J., Salmi M., Bono P., Hellman J., Leu T., Jalkanen S.;
RT "Cloning of vascular adhesion protein 1 reveals a novel
RT multifunctional adhesion molecule.";
RL J. Exp. Med. 188:17-27(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PNS;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Cell adhesion protein that participate in lymphocyte
CC recirculation by mediating the binding of lymphocytes to
CC peripheral lymph node vascular endothelial cells in an L-selectin-

CC independent fashion. Has a monoamine oxidase activity.
 CC -!- CATALYTIC ACTIVITY: $\text{RCH(2)NH(2)} + \text{H(2)O} + \text{O(2)} = \text{RCHO} + \text{NH(3)} + \text{H(2)O(2)}$.
 CC -!- COFACTOR: Binds 1 copper ion and 1 topaquinone per subunit.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -!- TISSUE SPECIFICITY: MOST STRONGLY EXPRESSED ON THE HIGH
 CC ENDOTHELIAL VENULES OF PERIPHERAL LYMPH NODES AND ON HEPATIC
 CC ENDOTHELIA.
 CC -!- PTM: Topaquinone (TPQ) is generated by copper-dependent
 CC autoxidation of a specific tyrosyl residue (By similarity).
 CC -!- PTM: N- and O-glycosylated.
 CC -!- SIMILARITY: Belongs to the copper/topaquinone oxidase family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; U39447; AAC50919.1; -.
 DR EMBL; AF067406; AAC25170.1; -.
 DR EMBL; BC050549; AAH50549.1; -.
 DR PIR; JC5234; JC5234.
 DR Genew; HGNC:550; AOC3.
 DR MIM; 603735; -.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0005886; C:plasma membrane; TAS.
 DR GO; GO:0008122; F:amine oxidase (copper-containing) activity; TAS.
 DR GO; GO:0005489; F:electron transporter activity; TAS.
 DR GO; GO:0009308; P:amine metabolism; TAS.
 DR InterPro; IPR000269; CuNH_oxidase.
 DR Pfam; PF01179; Cu_amine_oxid; 1.
 DR Pfam; PF02727; Cu_amine_oxidN2; 1.
 DR Pfam; PF02728; Cu_amine_oxidN3; 1.
 DR PRINTS; PR00766; CUDAOXIDASE.
 DR PROSITE; PS01164; COPPER_AMINE_OXID_1; 1.
 DR PROSITE; PS01165; COPPER_AMINE_OXID_2; 1.
 KW Oxidoreductase; Copper; TPQ; Glycoprotein; Transmembrane;
 KW Signal-anchor; Cell adhesion; Polymorphism; Metal-binding.
 FT DOMAIN 1 5 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 6 26 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 27 763 EXTRACELLULAR (POTENTIAL).
 FT MOD_RES 471 471 TOPAQUINONE (BY SIMILARITY).
 FT METAL 520 520 COPPER (POTENTIAL).
 FT METAL 522 522 COPPER (POTENTIAL).
 FT METAL 684 684 COPPER (POTENTIAL).
 FT BINDING 673 673 AMILORIDE (BY SIMILARITY).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 592 592 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 666 666 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT      VARIANT      317      317      Y -> H (in dbSNP:438287).
FT                                          /FTId=VAR_012064.
SQ      SEQUENCE     763 AA;  84621 MW;  58AD55605EC9D228 CRC64;

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Qy	263	QGGDGGEPSSLPHCPSPVSPSAQPPWTHPGQSQLFADLSREELTAVMRFLTQRLGPGGLVDAA	322
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Qy	323	QARPSDNCVFSVELQLPPKAAALAHLDRGSPPPAREALAIVFFGRQPQPNVSELVVGPLP	382
Db	88	QARPSDNCVFSVELQLPPKAAALAHLDRGSPPPAREALAIVFFGRQPQPNVSELVVGPLP	147
Qy	383	HPSYMRDVTVERHGGPLPYHRRPVLFQEYLDIDQMIFNRELPAQSGLLHHCCFYKHRGRN	442
Db	148	HPSYMRDVTVERHGGPLPYHRRPVLFQEYLDIDQMIFNRELPAQSGLLHHCCFYKHRGRN	207
Qy	443	LVTMTTAPRGLQSGDRATWFLYYNISGAGFFLHHVGLELLVNHKALDPARWTIQKVFIQ	502
Db	208	LVTMTTAPRGLQSGDRATWFLYYNISGAGFFLHHVGLELLVNHKALDPARWTIQKVFIQ	267
Qy	503	GRYYDSLAQLEAQFEAGLVNVVLIPDNGTGGSWSLKSPVPPGPAPPLQFYFQGPFRFSVQG	562
Db	268	GRYYDSLAQLEAQFEAGLVNVVLIPDNGTGGSWSLKSPVPPGPAPPLQFYFQGPFRFSVQG	327
Qy	563	SRVASSLWTFSGFLGAFSGPRIFDVRFQGERLVYEISLQEALAIYGGNSPAAMTTRYVDG	622
Db	328	SRVASSLWTFSGFLGAFSGPRIFDVRFQGERLVYEISLQEALAIYGGNSPAAMTTRYVDG	387
Qy	623	GFGMGKYTTPLTRGVDCPYLATYVDWHFLLESQAPKTIRDAFCVFEQNQGLPLRRHHS DL	682
Db	388	GFGMGKYTTPLTRGVDCPYLATYVDWHFLLESQAPKTIRDAFCVFEQNQGLPLRRHHS DL	447
Qy	683	YSHYFGGLAETVLVVRSMSTLLNYDYVWDTVFHPSGAIEIRFYATGYISSAFLFGATGKY	742
Db	448	YSHYFGGLAETVLVVRSMSTLLNYDYVWDTVFHPSGAIEIRFYATGYISSAFLFGATGKY	507
Qy	743	GNQVSEHTLGTVHTSHAHKVDLDVAGLENWVWAEDMVFVPMAPVPSPEHQLQRLQVTRK	802
Db	508	GNQVSEHTLGTVHTSHAHKVDLDVAGLENWVWAEDMVFVPMAPVPSPEHQLQRLQVTRK	567
Qy	803	LLEMEEQA AFLVGSATPRYLYLASNHSNKGWHPRGYRIQMLS FAGEPLPQNSSMARGFSW	862
Db	568	LLEMEEQA AFLVGSATPRYLYLASNHSNKGWHPRGYRIQMLS FAGEPLPQNSSMARGFSW	627
Qy	863	ERYQLAVTQRKEEPPSSSVFNQNDPWAPTVD FSDFINNETIAGKDLVAWVTAGFLHIPH	922
Db	628	ERYQLAVTQRKEEPPSSSVFNQNDPWAPTVD FSDFINNETIAGKDLVAWVTAGFLHIPH	687
Qy	923	AEDIPNTVTVGNGVGFFLRPNFFDEDPSFY SADS IYFRGDQDAGACEVNPLACL PQAAA	982
Db	688	AEDIPNTVTVGNGVGFFLRPNFFDEDPSFY SADS IYFRGDQDAGACEVNPLACL PQAAA	747
Qy	983	CAPDLPAFSGGGFSHN	998

Db

|||||
748 CAPDLEPAFSHGGFSHN 763

<220>

<223> Recombinant construct

<400> 20

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 1 5 10 15
 Ile Asn Ala Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys
 20 25 30
 Glu Gln Gln Asn Ala Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly
 35 40 45
 Leu Val Gln Pro Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr
 50 55 60
 Glu Glu His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys
 65 70 75 80
 Lys Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp
 85 90 95
 Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala
 100 105 110
 Asp Lys His Asn Met Leu Gly Gly Ser Pro Lys Glu Arg Ala Glu Ile
 115 120 125
 Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg
 130 135 140
 Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser
 145 150 155 160
 Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Ser His Lys
 165 170 175
 Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr
 180 185 190
 Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala
 195 200 205
 Phe Pro Lys Leu Val Ser Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln
 210 215 220
 Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln
 225 230 235 240
 Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Gln
 245 250 255
 Ser Gln Glu Ala Leu Phe Gln Gly Gly Asp Gly Gly Glu Pro Ser Gln
 260 265 270
 Leu Pro His Cys Pro Ser Val Ser Pro Ser Ala Gln Pro Trp Thr His
 275 280 285
 Pro Gly Gln Ser Gln Leu Phe Ala Asp Leu Ser Arg Glu Glu Leu Thr
 290 295 300
 Ala Val Met Arg Phe Leu Thr Gln Arg Leu Gly Pro Gly Leu Val Asp
 305 310 315 320
 Ala Ala Gln Ala Arg Pro Ser Asp Asn Cys Val Phe Ser Val Glu Leu
 325 330 335
 Gln Leu Pro Pro Lys Ala Ala Ala Leu Ala His Leu Asp Arg Gly Ser
 340 345 350
 Pro Pro Pro Ala Arg Glu Ala Leu Ala Ile Val Phe Phe Gly Arg Gln
 355 360 365
 Pro Gln Pro Asn Val Ser Glu Leu Val Val Gly Pro Leu Pro His Pro
 370 375 380
 Ser Tyr Met Arg Asp Val Thr Val Glu Arg His Gly Gly Pro Leu Pro
 385 390 395 400
 Tyr His Arg Arg Pro Val Leu Phe Gln Glu Tyr Leu Asp Ile Asp Gln
 405 410 415

signal

signal peptide

fusion partner

quar

SC
leavage

SSAD

Met Ile Phe Asn Arg Glu Leu Pro Gln Ala Ser Gly Leu Leu His His
 420 425 430
 Cys Cys Phe Tyr Lys His Arg Gly Arg Asn Leu Val Thr Met Thr Thr
 435 440 445
 Ala Pro Arg Gly Leu Gln Ser Gly Asp Arg Ala Thr Trp Phe Gly Leu
 450 455 460
 Tyr Tyr Asn Ile Ser Gly Ala Gly Phe Phe Leu His His Val Gly Leu
 465 470 475 480
 Glu Leu Leu Val Asn His Lys Ala Leu Asp Pro Ala Arg Trp Thr Ile
 485 490 495
 Gln Lys Val Phe Tyr Gln Gly Arg Tyr Tyr Asp Ser Leu Ala Gln Leu
 500 505 510
 Glu Ala Gln Phe Glu Ala Gly Leu Val Asn Val Val Leu Ile Pro Asp
 515 520 525
 Asn Gly Thr Gly Gly Ser Trp Ser Leu Lys Ser Pro Val Pro Pro Gly
 530 535 540
 Pro Ala Pro Pro Leu Gln Phe Tyr Pro Gln Gly Pro Arg Phe Ser Val
 545 550 555 560
 Gln Gly Ser Arg Val Ala Ser Ser Leu Trp Thr Phe Ser Phe Gly Leu
 565 570 575
 Gly Ala Phe Ser Gly Pro Arg Ile Phe Asp Val Arg Phe Gln Gly Glu
 580 585 590
 Arg Leu Val Tyr Glu Ile Ser Leu Gln Glu Ala Leu Ala Ile Tyr Gly
 595 600 605
 Gly Asn Ser Pro Ala Ala Met Thr Thr Arg Tyr Val Asp Gly Gly Phe
 610 615 620
 Gly Met Gly Lys Tyr Thr Thr Pro Leu Thr Arg Gly Val Asp Cys Pro
 625 630 635 640
 Tyr Leu Ala Thr Tyr Val Asp Trp His Phe Leu Leu Glu Ser Gln Ala
 645 650 655
 Pro Lys Thr Ile Arg Asp Ala Phe Cys Val Phe Glu Gln Asn Gln Gly
 660 665 670
 Leu Pro Leu Arg Arg His His Ser Asp Leu Tyr Ser His Tyr Phe Gly
 675 680 685
 Gly Leu Ala Glu Thr Val Leu Val Val Arg Ser Met Ser Thr Leu Leu
 690 695 700
 Asn Tyr Asp Tyr Val Trp Asp Thr Val Phe His Pro Ser Gly Ala Ile
 705 710 715 720
 Glu Ile Arg Phe Tyr Ala Thr Gly Tyr Ile Ser Ser Ala Phe Leu Phe
 725 730 735
 Gly Ala Thr Gly Lys Tyr Gly Asn Gln Val Ser Glu His Thr Leu Gly
 740 745 750
 Thr Val His Thr His Ser Ala His Phe Lys Val Asp Leu Asp Val Ala
 755 760 765
 Gly Leu Glu Asn Trp Val Trp Ala Glu Asp Met Val Phe Val Pro Met
 770 775 780
 Ala Val Pro Trp Ser Pro Glu His Gln Leu Gln Arg Leu Gln Val Thr
 785 790 795 800
 Arg Lys Leu Leu Glu Met Glu Glu Gln Ala Ala Phe Leu Val Gly Ser
 805 810 815
 Ala Thr Pro Arg Tyr Leu Tyr Leu Ala Ser Asn His Ser Asn Lys Trp
 820 825 830
 Gly His Pro Arg Gly Tyr Arg Ile Gln Met Leu Ser Phe Ala Gly Glu
 835 840 845
 Pro Leu Pro Gln Asn Ser Ser Met Ala Arg Gly Phe Ser Trp Glu Arg
 850 855 860
 Tyr Gln Leu Ala Val Thr Gln Arg Lys Glu Glu Glu Pro Ser Ser Ser

[illegible]